

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: September 4, 2002, 16:16:02 : Search time 172.18 Seconds  
(without alignments)  
221.041 Million cell updates/sec

Title: US-09-052-089a-4  
Perfect score: 1075  
Sequence: 1 KTIINKLRFEDLAQEEENVLD.....DLQADQETSLRKSDPP 220

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :  
1: SPREMBL\_19:\*  
2: sp.archaea:\*  
3: sp.bacteria:\*  
4: sp.fungi:\*  
5: sp.human:\*  
6: sp.invertebrate:\*  
7: sp.mammal:\*  
8: sp.mhc:\*  
9: sp.organelle:\*  
10: sp.plant:\*  
11: sp.podent:\*  
12: sp.virus:\*  
13: sp.vertibrate:\*  
14: sp.unclassified:\*  
15: sp.virus:\*  
16: sp.bacteriap:\*  
17: sp.archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1045	97.2	470	11	Q9CP4 mus musculu
2	1045	97.2	470	11	Q08854 mus musculu
3	920	85.6	469	4	Q9BWP2 Q9BWP2 homo sapien
4	906	84.3	469	4	000467 000467 homo sapien
5	740	68.8	223	11	Q922M8 0922M8 mus musculu
6	522	48.6	433	13	Q9YGN2 09YGN2 fugu rubrip
7	180	16.7	2139	5	Q07569 007569 entamoeba h
8	176	16.4	2473	11	Q9Q284 09Q284 mus musculu
9	175.5	16.3	1827	5	Q20042 020042 caenorhabdi
10	175.5	16.3	1885	5	Q950G9 0950G9 caenorhabdi
11	175.5	16.3	1898	5	Q950H0 0950H0 caenorhabdi
12	175	16.3	324	11	Q9BCN8 09BCN8 mus musculu
13	170.5	15.9	574	4	Q9H810 09H810 homo sapien
14	169	15.7	397	11	Q999P7 0999P7 cavia porce
15	168	15.6	484	6	Q28713 028713 oryctolagus
16	168	15.6	588	4	014729 014729 homo sapien

17	167	15.5	2138	5	Q9XZE3 09XZE3 amoeba prot
18	166	15.4	1578	10	Q9AV25 09AV25 oryza sativ
19	166	15.4	1958	5	Q96062 096062 dugesia jap
20	166	15.4	2017	5	Q94992 094992 drosophila
21	166	15.4	2056	5	Q9W0W8 09W0W8 drosophila
22	166	15.4	2057	5	Q94987 094987 drosophila
23	165.5	15.4	1447	11	Q9QYT2 09QYT2 mus musculu
24	165.5	15.4	1487	11	Q9QYT3 09QYT3 mus musculu
25	165.5	15.4	1871	5	Q9NCL3 09NCL3 drosophila
26	165	15.3	1743	5	Q96063 096063 dugesia jap
27	165	15.3	1941	5	Q26079 026079 placopecten
28	165	15.3	1950	5	Q26080 026080 placopecten
29	164.5	15.3	746	5	Q25561 025561 naegleria f
30	164.5	15.3	2501	5	Q9NCW7 09NCW7 drosophila
31	164	15.3	1940	5	Q9UT63 09UT63 pecten maxi
32	163	15.2	1313	10	Q9XIP6 09XIP6 arabidopsis
33	163	15.2	1790	3	Q07380 007380 saccharomyc
34	162	15.1	692	5	Q96720 096720 dermatophag
35	162	15.1	826	13	Q9YHDS 09YHDS rana catesb
36	162	15.1	1219	5	Q9NJ23 09NJ23 aequipecten
37	162	15.1	1229	5	Q9NJ22 09NJ22 aequipecten
38	162	15.1	1243	5	Q9NJ21 09NJ21 aequipecten
39	162	15.1	1253	5	Q9NJ20 09NJ20 aequipecten
40	162	15.1	1951	5	Q17042 017042 aequipecten
41	161	15.0	296	4	Q16085 016085 homo sapien
42	160.5	14.9	1957	5	Q04010 004010 onchocerca
43	160.5	14.9	1963	5	Q02244 002244 caenorhabdi
44	160	14.9	924	5	Q15738 015738 dictyostell
45	160	14.9	948	4	Q9UIK7 09UIK7 homo sapien

## ALIGNMENTS

RESULT	ID	Q9CP4	Q9CP4	PRELIMINARY;	PRT;	470 AA.
AC	Q9CP4					
DT	01-JUN-2001	(TEMBUREL 17, Created)				
DT	01-JUN-2001	(TEMBUREL 17, Last sequence update)				
DT	01-DEC-2001	(TEMBUREL 19, Last annotation update)				
DE	TRAF-INTERACTING PROTEIN.					
GN	TRAF.					
OS	Mus musculus (Mouse).					
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;					
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.					
OX	NCBI_TaxID=10090;					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RC	STRAIN=C57BL/6J; TISSUE=EMBRYO;					
RX	MEDLINE=21085660; Pubmed=11217851;					
RA	Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,					
RA	Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,					
RA	Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamakata I.,					
RA	Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,					
RA	Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,					
RA	Fleischmann W., Gaasterland T., Gissi C., King B., Kochwa H.,					
RA	Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,					
RA	Schirral L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,					
RA	Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,					
RA	Blake J., Boffelli D., Bojunga N., Carinci P., de Bonaldo M.F.,					
RA	Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,					
RA	Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya K., Lee N.H.,					
RA	Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,					
RA	Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,					
RA	Sasakawa H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,					
RA	Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,					
RA	Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,					
RA	Hayashizaki Y.,					
RT	"Functional annotation of a full-length mouse cDNA collection.";					
RL	Nature 409:685-690(2001).					
CC	-i- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.					
DR	EMBL; AK012948; BAB28567.1; -					

DR EMBL: AK012786; BAB28469.1; -  
DR MGD: MGI:1096377; Traip.  
DR InterPro: IPR001841; Znf\_r1ng.  
DR Pfam: PF00097; zf-C3HC4; 1.  
DR SMART: SM00184; RING; 1.  
DR zinc-finger.  
KW  
SQ SEQUENCE 470 AA; 53149 MW; EBFABC49A9F4BF2E CRC64;

Query Match 97.2%; Score 1045; DB 11; Length 470;  
Best Local Similarity 100.0%; Pred. No. 3.6e-50;  
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KTIINKLFEDLAOEENVLDAEFLKNELDYSKAQLSQDKRKRDSQAIIIDTLRPTLEERN 60  
DB 56 KTIINKLFEDLAOEENVLDAEFLKNELDYSKAQLSQDKRKRDSQAIIIDTLRPTLEERN 115  
QY 61 ATVESLONALKAMLCSTLKKQMKFLEQRDDETKQAREEAHRLCKMKTMEQIETLLQS 120  
DB 116 ATVESLONALKAMLCSTLKKQMKFLEQRDDETKQAREEAHRLCKMKTMEQIETLLQS 175  
QY 121 ORSEVEEMIRDMGVGOSAVEQLAVYCVSLKKEYENLKEARKATGELADRLKKDLVSSRSK 180  
DB 176 ORSEVEEMIRDMGVGOSAVEQLAVYCVSLKKEYENLKEARKATGELADRLKKDLVSSRSK 235  
QY 181 LKTLNTELDQAKLELRSQKDLQASADDEITSLRKK 215  
DB 236 LKTLNTELDQAKLELRSQKDLQASADDEITSLRKK 270  
RESULT 2  
ID 008854 PRELIMINARY; PRT; 470 AA.  
AC 008854;  
DT 01-JUL-1997 (TREMblrel. 04, Created)  
DT 01-JUL-1997 (TREMblrel. 04, Last sequence update)  
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)  
DE MTRIP.  
GN TRAP OR MTRIP.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=97258620; PubMed=9104814;  
RA Lee S.Y., Lee S.Y., Choi Y.;  
RT "TRAF-interacting protein (TRIP): a novel component of the tumor  
RT necrosis factor receptor (TNFR)- and CD30-TRAF signaling complexes  
RT that inhibits TRAF2-mediated NF-kappaB activation.";  
RL J. Exp. Med. 185:1275-1285(1997).  
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.  
DR EMBL: U77844; AAB52994.1; -  
DR MGD: MGI:1096377; Traip.  
DR InterPro: IPR001841; Znf\_r1ng.  
DR Pfam: PF00097; zf-C3HC4; 1.  
DR SMART: SM00184; RING; 1.  
DR zinc-finger.  
KW  
SQ SEQUENCE 470 AA; 53191 MW; 00FD705B52645133 CRC64;

Query Match 97.2%; Score 1045; DB 11; Length 470;  
Best Local Similarity 100.0%; Pred. No. 3.6e-50;  
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KTIINKLFEDLAOEENVLDAEFLKNELDYSKAQLSQDKRKRDSQAIIIDTLRPTLEERN 60  
DB 56 KTIINKLFEDLAOEENVLDAEFLKNELDYSKAQLSQDKRKRDSQAIIIDTLRPTLEERN 115  
QY 61 ATVESLONALKAMLCSTLKKQMKFLEQRDDETKQAREEAHRLCKMKTMEQIETLLQS 120  
DB 116 ATVESLONALKAMLCSTLKKQMKFLEQRDDETKQAREEAHRLCKMKTMEQIETLLQS 175

QY 121 ORSEVEEMIRDMGVGOSAVEQLAVYCVSLKKEYENLKEARKATGELADRLKKDLVSSRSK 180  
DB 176 ORSEVEEMIRDMGVGOSAVEQLAVYCVSLKKEYENLKEARKATGELADRLKKDLVSSRSK 235  
QY 181 LKTLNTELDQAKLELRSQKDLQASADDEITSLRKK 215  
DB 236 LKTLNTELDQAKLELRSQKDLQASADDEITSLRKK 270

RESULT 3  
ID 09BWF2 PRELIMINARY; PRT; 469 AA.  
AC 09BWF2;  
DT 01-JUN-2001 (TREMblrel. 17, Created)  
DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)  
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)  
DE TRAF INTERACTING PROTEIN.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=LUNG CARCINOMA;  
RA Strausberg R.;  
RL Submitted (NOV-2000) to the EMBL/Genbank/DBJ databases.  
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.  
DR EMBL: BC000310; AA000310.1; -  
DR InterPro: IPR001841; Znf\_r1ng.  
DR Pfam: PF00097; zf-C3HC4; 1.  
DR SMART: SM00184; RING; 1.  
DR zinc-finger.  
KW  
SQ SEQUENCE 469 AA; 53294 MW; B9EF3808FBC5965B CRC64;

Query Match 85.6%; Score 920; DB 4; Length 469;  
Best Local Similarity 87.0%; Pred. No. 2.5e-43;  
Matches 187; Conservative 18; Mismatches 10; Indels 0; Gaps 0;

QY 1 KTIINKLFEDLAOEENVLDAEFLKNELDYSKAQLSQDKRKRDSQAIIIDTLRPTLEERN 60  
DB 56 KTIINKLFEDLAOEENVLDAEFLKNELDYVRAQLSQDKRKRDSQAIIIDTLRPTLEERN 115  
QY 61 ATVESLONALKAMLCSTLKKQMKFLEQRDDETKQAREEAHRLCKMKTMEQIETLLQS 120  
DB 116 ATVESLONALKAMLCSTLKKQMKYLEQDDDETKQAREEAHRLCKMKTMEQIETLLQS 175  
QY 121 ORSEVEEMIRDMGVGOSAVEQLAVYCVSLKKEYENLKEARKATGELADRLKKDLVSSRSK 180  
DB 176 ORSEVEEMIRDMGVGOSAVEQLAVYCVSLKKEYENLKEARKATGELADRLKKDLVSSRSK 235  
QY 181 LKTLNTELDQAKLELRSQKDLQASADDEITSLRKK 215  
DB 236 LKTLNTELDQAKLELRSQKDLQASADDEITSLRKK 270

RESULT 4  
ID 000467 PRELIMINARY; PRT; 469 AA.  
AC 000467;  
DT 01-JUL-1997 (TREMblrel. 04, Created)  
DT 01-JUL-1997 (TREMblrel. 04, Last sequence update)  
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)  
DE HTRIP.  
GN HTRIP.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=97258620; PubMed=9104814;  
RA Lee S.Y., Lee S.Y., Choi Y.;



RC STRAIN-HMI:IMSS;  
 RA Gullien N.;  
 RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: L03534; AAB48065.1; -  
 DR HSPR: P08799; 1MND.  
 DR InterPro: IPR000048; IQ.  
 DR InterPro: IPR001609; myosin\_head.  
 DR Pfam: PF00612; IQ; 2.  
 DR Pfam: PF00063; myosin\_head.1.  
 DR PRINTS: PR00193; MYOSINHEAVY.  
 DR PRODOM: PD000355; myosin\_head.1.  
 DR SMART: SM00242; MISC; 1.  
 DR SEQUENCE 2139 AA; 245225 MW; C68307341DB51DD1 CRC64;

Query Match 16.7%; Score 180; DB 5; Length 2139;  
 Best Local Similarity 27.6%; Pred. No. 0.031;

Matches 60; Conservative 52; Mismatches 77; Indels 28; Gaps 7;

QY 11 LAOEENYLAEPFLKNEIDSVKQLSQK-----DREKDSQAIIIDTLRDLERNATV 63  
 DB 1671 VAQEEK-----QRLSDIAELKEQLEQERTAAANAERKKIQAELEDEVKKNLEDTVNR 1726  
 QY 64 ESL--QNALNKAEMLCSTLKKOMKFLERODEYKQAREEAHRLCKMKTMEQIELLSQ 121  
 DB 1727 EKLVAKNSENDAEI--DSLKEEKKALE--DEIEKITDDNKLKLS-----EIDSLDRKY 1775  
 QY 122 RSEVEEMIRDMGVGQSAVEOLAAYCVSLKKEYENLKEARKATGELADRLKKDLVSSRKL 181  
 DB 1776 NALDSKDSVDYKMEKRFODELKTVDKDALETETKKNHAEYTRKNG--RLKEEAAEVQVRL 1831  
 QY 182 KTLNTELDQAKLELSAQKDSAQDOETISLRKSSD 218  
 DB 1832 EALQKNLDLAQGEKAKATKDYRADGELKSLMNELD 1868

RESULT 8  
 ID 090284 PRELIMINARY; PRT; 2473 AA.  
 AC 090284;  
 DT 01-MAY-2000 (TREMblrel. 13, Created)  
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)  
 DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)  
 DE LEK1 (FRAGMENT).  
 GN 6530404A22RIK.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;  
 OC NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99303627; Pubmed=10373470;  
 RA Goodwin R.L., Pabon-Pena L.M., Foster G.C., Bader D.;  
 RT "The cloning and analysis of LEK1 identifies variations in the  
 RT LEK/centromere protein F/miostin gene family";  
 RL J. Biol. Chem. 274:18597-18604(1999).  
 DR EMBL: AF194970; AAF07196.1; -  
 DR MGD: MGI:1915046; 6530404A22RIK.  
 FT NON\_TER 1  
 SO SEQUENCE 2473 AA; 281903 MW; 504E91A1A150A3E5 CRC64;

Query Match 16.4%; Score 176; DB 11; Length 2473;  
 Best Local Similarity 23.3%; Pred. No. 0.059;

Matches 60; Conservative 60; Mismatches 90; Indels 48; Gaps 6;

QY 1 KTIINKLFFDLAEEEN---VLDAPFLKNEIDSVKQLSQKREKDSQAIIIDTLRDTL 56  
 DB 1629 KDVTLELERERSEENQELALIDSENILKAVERTLKQKDKMTSLRIFELDLVTVRER 1668  
 QY 57 EERNAVESIQNALNKAEMLCSTLKKOMKFLER-----ODETQAREEA 101  
 DB 1689 ENLAKOLOEKOSRVSELDERSLSRLLEKEKQARVOMEEDSKSAMLTQMLKELREEV 1748

QY 102 HRLCKMKTMEQIELLSQSRSEVEEMIRDMGVGQSAVEOLAAYCVSLKKEYENLKEARK 161  
 DB 1749 AALCNDOETLKAQDSIDQPOEEVNHLL-----KSSIRLKVIIIDAEKKNHILDLK 1801  
 QY 162 ATGELADRLK-----KDLV---SSRSKLTNTELDQAKLELSAQKDLO 203  
 DB 1802 ESKHHADILKRVENLRLQELILSEKNNMIFQAEKSKAEIQTLKSEIQMAQNLQDLLELI 1861  
 QY 204 SADOE-----ITSLKKSD 217  
 DB 1862 STRSENNELIKELKEOE 1879

RESULT 9  
 ID 020042 PRELIMINARY; PRT; 1827 AA.  
 AC 020042;  
 DT 01-NOV-1996 (TREMblrel. 01, Created)  
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)  
 DE HYPOTHEICAL 215.1 KDA PROTEIN.  
 GN F35D11.1.  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematozoa; Chromadorea; Rhabditida; Rhabditidae;  
 OC Rhabditidae; Pelodierinae; Caenorhabditis.  
 OC NCBI\_TaxID=6239;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BRISTOL N2;  
 RX MEDLINE=99069613; Pubmed=9851916;  
 RA None;  
 RT "Genome sequence of the nematode C. elegans: a platform for  
 RT investigating biology. The C. elegans Sequencing Consortium.";  
 RL Science 282:2012-2018(1998).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BRISTOL N2;  
 RA Fulton L., Wilson R.;  
 RT "The sequence of C. elegans cosmid F35D11.";  
 RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BRISTOL N2;  
 RA Waterston R.;  
 RT "Direct Submission";  
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: U29381; AAA68757.1; -  
 KW Hypothetical protein.  
 SO SEQUENCE 1827 AA; 215143 MW; 551C28858452A0FA CRC64;

Query Match 16.3%; Score 175.5; DB 5; Length 1827;  
 Best Local Similarity 25.3%; Pred. No. 0.047;  
 Matches 58; Conservative 61; Mismatches 79; Indels 31; Gaps 8;

QY 5 NKLFFDLAEEENYLD-----AEFLKNEIDSVKQLSQKREKDSQAIIIDTLR--- 53  
 DB 669 NEKTDARAKNDALLEVATVQOEYEBOLKELBEMNRGOEKEEBADRLALDDLGNF 728  
 QY 54 ---DLEERNATVESIQNALNKAEMLCSTLKKOM--FLERODEYKQAREEAHRLCKM 108  
 DB 729 DKLINELKQGVTVDSINBEI-----SLKBDLNKSEKREKELRLMELEBKNAEM 781  
 QY 109 KTMEOIEL-LIOSORSEVEEMIRDMGVGQSAVEOLAAYCVSLKKEYENLKEARKATGELA 167  
 DB 782 KEEVEYVLAQEKDROGVENNGKEC--EARMNELTGIHEMLMEHDLVYDLHTEEV 838  
 QY 168 DRLLKDLVSSRKLKTLNTELDQAKLELSAQKDSAQDOETISLRKSSD--ITSLLKK 215  
 DB 839 ERLKEKM--RKLELEKNBNDGDRAEWSNBRNRLSSKNEAVTELOER 884

RESULT	ID	PRELIMINARY	PRT	AA
10	0950G9			
	0950G9	PRELIMINARY	PRT	1865 AA.
AC	0950G9			
DT	01-DEC-2001 (TREMBLrel. 19, Created)			
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)			
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
DE	HYPOHETICAL 221.7 KDA PROTEIN.			
GN	P35D11.11.			
OS	Caenorhabditis elegans.			
OC	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea			
OC	Rhabditidae; Peloiderinae; Caenorhabditis.			
OX	NCBI_Taxid=6239;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-BRISTOL N2;			
RX	MEDLINE=99069613; PubMed=9851916;			
RA	None;			
RT	"Gene sequence of the nematode C. elegans: a platform for			
RT	investigating biology. The C. elegans Sequencing Consortium.",			
RL	Science 282:2012-2018(1998).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-BRISTOL N2;			
RA	Fulton L., Wilson R.;			
RT	"The sequence of C. elegans cosmid F35D11.";			
RL	Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-BRISTOL N2;			
RA	Waterston R.;			
RT	"Direct Submission.";			
RL	Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.			
DR	EMBL: U29381; AAI02511.1.; -			
KW	Hypothetical protein.			
SQ	SEQUENCE 1865 AA; 221745 MW; 28B331A4C7D1F00C CRC64;			

Query Match	16.3%	Score 175.5	DB 5	Length 1885
Best Local Similarity	25.3%	Pred. No. 0.049		
Matches 58	Conservative 61	Mismatches 79	Indels 31	Gaps
QY	5	NKLFEDLAQEEENVLD-----AEFLKNELDVSKAQLISOKDRKRSQAIIDTLR---	53	
Db	669	NEKYDARKKNDALLLEDVATWQEKYEOLKMEEMNRROQEKEREEDRLALLDDRCNF	728	
QY	54	-----DTLEERNATVESIONALKAMLCSTLKKOM-KLEEQODETKQAREAHRLKCM	108	
Db	729	DKLTNELKQKGVTVLSLMEEI-----SSLKEOLNKSKEKEKEELIRMEELQKNEAM	781	
QY	109	KTMEQIEI-LLOSQRSEVEEMIRDMGVCSQAVEQLAVCVSLKEEYENLEAKRKATGELA	167	
Db	782	KEEYEVKIQGLAEKKDROGVENFGEK---EARNNELTKIHIMLMIEBHDLQVYHLLTEEV	838	
QY	168	DRKKDVLVSSRSKLTMTLTIELDQAKLELRSAQKDIQSADQF-TTSLIRK	215	
Db	839	ERLKEKM---RKLEKLTNEQNDGDRAEWSNERNRRLSSKNEAYTELQER	884	
RESULT	11			
Q95OHO				
ID	Q95OHO	PRELIMINARY:	PRT:	1898 AA.
AC	Q95OHO			
DT	01-DEC-2001 (TREMBLrel. 19, Created)			
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)			
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
DE	HYPOTHETICAL 223.4 KDA PROTEIN.			
GN	F35D11.11.			
OS	Caenorhabditis elegans.			
OC	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabdilitida; Rhabditoidea;			
OC	Rhabdilitidae; Pelodierinae; Caenorhabditis.			
NCBI	taxid=6239;			
RM	[1]			

RP SEQUENCE FROM N.A..  
RC STRAIN-BRISTOL N2;  
RX MEDLINE=99069613; PubMed=9851916;  
RA None;  
RT "Genome sequence of the nematode *C. elegans*: a platform for  
RT investigating biology. The *C. elegans* Sequencing Consortium.";  
RL Science 282:2012-2018(1998).  
RN [2]  
RP SEQUENCE FROM N.A..  
RC STRAIN-BRISTOL N2;  
RA Fulton L., Wilson R.;  
RT "The sequence of *C. elegans* cosmid F35d11.";  
RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A..  
RC STRAIN-BRISTOL N2;  
RA Waterston R.;  
RT "Direct Submission.";  
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL: U29381; AAL02510.1; -.  
KW Hypothetical protein.  
SO SEQUENCE 1898 AA; 223357 MW; 79190ACBBDB6DE6C CRC64;

```

Query Match          16.3%; Score 175.5; DB 5; Length 1898;
Best Local Similarity 25.3%; Pred. No. 0.049; Indels 31; Gaps 8;
Matches 58; Conservative 61; Mismatches 79; Indels 31; Gaps 8;

OY 5 NKLFPDLAOEENVD-----AFLKNEIDSVKAOISOKDKREKRSOAILIDPLR---53
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 669 NEKYDADARKNDALLEEDVATWQEKTEQGLKMLEENNRGQEKEREEDRALDDLRGNF 728
OY 54 ---DTLEERNATVESLONALKKAMLCSTLKKQ-KPLEQRQDQETKQAREEAHRLKCM 108
   | : : : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 729 DKLITELKQKQVTVDSLNDKEI-----SLKQELNKSSEKKEKELLRLREELEOKNEAM 781
OY 109 KTMDEIL-LLOSQSEVEPEEMIRDMGQGSNAVEQALVCSLSKREYENIKERKATGELA 167
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 782 KEVEEVKLOLKERDQGVENFGEC--EARNELTKIHEMLMEHDDOLKVLHPLTEBEV 838
OY 168 DLRLKDLVSSRSKLTNTLTDLOAKTELRSAQKDQSDAOE-ITSLRKK 215
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 839 ERLKEM---KRELEKLNQDNGDRAEMSNENKRNLRSSKNENAVTELQER 864

RESULT 12
O9EQN8
ID O9EQN8 PRELIMINARY: PRT: 324 AA.
AC O9EQN8:
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE MITOSIN (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
OX NCBI_Taxid=10090.
RN [1]
RP SEQUENCE FROM N.A.
RA Qian M., Lin D., Zhu X.:
RT "Evolution of the internal repeat of mtosin.";
RL Submitted (SEP-1999) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF182407; AACG3426.1; -
DR InterPro: IPR000533; Tropomyosin.
DR PRINTS: PRD0194; TROPOMYOSIN.
FT NON_TER 1
FT NON_TER 324
FT NON_TER 324
SQ SEQUENCE 324 AA; 37896 MW; A64CD5A55E1D7D7D CRC64;

```

```
QY 1 KTIINKLFFDLAEEEN-----VLDAEFLKNELDVSKAQLSQRKREKRDQAIIIDTLRDTL 56
D 25 KDKVENLERLEJMESENELAIIIDSENKAEVETLKAQMDMAKSLRFLFDLVNVRSE 84
QY 57 EERNATVESLONALNKAMLCSTLKKOMKFLERODETKQAREAHN-----LKCKM 108
D 85 ENLAKQLOEKOSRVSELDCESSLR-----SLSEEKQARVOMERDSKAMLMLOTQL 137
QY 109 KTM-BOJELL-----LOSQRSEVEEMIRDMGVOSANEOALAVYCVSLKRE-----YENLK 157
D 138 KELLEVAALINDQETLKAQOSLDQEGEEVHLKSSIOKLKVNHDADKKKCHILEQL 197
QY 158 EARRATGELADR-----LKKDLVSSRSKLTNTLTDQAKLELSAQKLOSDAQ-----207
D 198 ESKNHADLFKRVENLBQELMLSEKNKHLIFQAENSAELIQTLTETLQTMQNDQDEL 257
QY 208 EITSLRKSDD 218
D 258 ELTMTSRSEKEN 268
```

```
RESULT 13
Q9H810 PRELIMINARY: PRT: 574 AA.
AC Q9H810;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DE 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
DE CDNA FLJ13615 F1S, CLONE PLACE1010896, WEAKLY SIMILAR TO NUFI
DE PROTEIN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiinae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA;
RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
RA Megatsuna M., Hosoliri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
RA Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuno Y.,
RA Ninomiya K., Iwayanagi T.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (MIG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AK023677; BABI4636.1;
SQ SEQUENCE 574 AA; 67926 MW; 97EF904DD4EB9EA5 CRC64;
```

```
Query Match 15.9%; Score 170.5; DB 4; Length 574;
Best Local Similarity 22.3%; Pred. No. 0.03; Indels 63; Gaps 8;
Matches 59; Conservative 52; Mismatches 90;
```

```
QY 1 KTIINKL-FFDLAEEENVLDAEFLKNELDVSKAQLSQRKREKRDQAIIIDTLRDT 55
D 88 KTKVMKLENELEMAQSGAGSDTRFLRNEIQCLEKQLEKQRELEDEMEKELEKRYNEQ 147
QY 56 LEEFNATVESLONAL-----NKAEMLCSTLKKOMKFLERODE--TKQAREAHRLK 105
D 148 LALNEEAENENSKLRRENKRLKKNQOLCDDIIDYQKQISQKRETLSTRGSDYSRQ 207
QY 106 CKMKT-----EQIELLOSQRSEVEEMIRDMGVOSAVQALVYCVSL 149
D 208 LSKNNTLQYLDLQTLTEANKEIEVQNDMRKNLEESVEM-----EKM 253
QY 150 KKEYENLEKARKATGELADRLK-----DIVSSRSK-----LKTLTMLDQA 191
D 254 TDEVNRKMKATVHQNDVNDIDQKKKNDHNYQQLVQELTDLKSKNEEDDPINVAVAKYEW 313
QY 192 KLELRSAQKLOSDAQEITSLRKK 215
```

D 314 KLILSKDEIIEYQOMLNLREK 337

```
RESULT 14
Q99PR7 PRELIMINARY: PRT: 397 AA.
AC Q99PR7;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DE 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE ENTEROPHILIN-2L (FRAGMENT).
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CRL (BFA) BR;
RA Gassama A., Hulin-Matsuda F., Li R.Y., Nauze M., Ragab A.,
RA Delagebeaudouf C., Simon M.F., Fauvel J., Chap H.;
RT "Enterophilins, a new family of leucine zipper proteins bearing a
RT B30.2 domain and associated with enterocyte differentiation.";
RL J. Biol. Chem. 0:0-0(2001).
DR EMBL: AF126831; AAK02014.1;
DR HSP; P01100; IPOS.
DR InterPro: IPR001870; Gamma_carboxylase.
DR InterPro: IPR003345; M_repeat.
DR InterPro: IPR003877; SPRY.
DR InterPro: IPR003878; SPRY_domain.
DR Pfam: PF02370; M; 8.
DR Pfam: PF00622; SPRY; 1.
DR SMART: SM00449; SPRY; 1.
FT NON_TER 1
SQ SEQUENCE 397 AA; 48062 MW; CA78B87B8A039C62 CRC64;
```

```
Query Match 15.7%; Score 169; DB 11; Length 397;
Best Local Similarity 25.1%; Pred. No. 0.026;
Matches 53; Conservative 47; Mismatches 89; Indels 22; Gaps 4;
```

```
QY 10 DLAOEENVL-DAEFLKNELDVSKAQLSQRKREKRDQAIIIDTLRDLLEERNATVESLQ 67
D 4 DQLEKEEQLEKKEKETLQTKHDKGKEQRLKEKETLQTEHNDQLEKEEQLRKDKETLQ 63
QY 68 NALNKAMLCSTLKKOMKFLERODETKQAREAHNRLKCKMKTMEQIELLOSQRSEVE 127
D 64 TKHQ-----LKEEETLQTKHDKQLEKEEQLR-----KQKETLQTKHDKQLEKEEQ 110
QY 128 MIRMGVOSAVEQLAVYCVSLKKEYENLEKARKATGELADRLKDLVSSRSKLTNTL 187
D 111 LRKDKETLQTKHQ-----LKEEKEQLRKDKETLQTKHDKQLEKEEQLRKDKETLQTK 163
QY 188 LDAQKLELRSAQKLOSDAQEITSLRKSDD 218
D 164 HDQLEKEEQLRKDKETLQTEHNDQLEKEEQID 194
RESULT 15
Q28713 PRELIMINARY: PRT: 484 AA.
AC Q28713;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE SMOOTH MUSCLE MYOSIN HEAVY CHAIN (LIGHT MEROMYOSIN) (FRAGMENT).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=88124972; PubMed=3422477;
RA Nagai R., Larson D.M., Periasamy M.;
```





DR InterPro: IPR002928; Myosin\_tail.  
 DR Pfam: PF00612; IQ; 1.  
 DR Pfam: PF0063; myosin\_head; 1.  
 DR Pfam: PF02736; Myosin\_N; 1.  
 DR Pfam: PF01576; Myosin\_tail; 1.  
 DR PRINTS: PR00193; MYOSINHEAVY.  
 DR ProDom: PD000355; myosin\_head; 1.  
 DR SMART: SM00015; IQ; 1.  
 DR SMART: SM00242; MYSC; 1.  
 DR PROSITE: PSS0096; IQ; 1.  
 SQ SEQUENCE 2017 AA; 232089 MW; 8C76FEF2EBD02EBE CRC64;

Query Match 15.4%; Score 166; DB 5; Length 2017;  
 Best Local Similarity 25.2%; Pred. No. 0.17;  
 Matches 61; Conservative 47; Mismatches 96; Indels 38; Gaps 8;

QY 1 KTIINKLFFDLQAEENVDAE--FLKNELDSYKAQLSQDKREKRSQ-----AI 48  
 DB 1263 KTVLEK-----AKGTLEENADLATELRVSVSSRQENDRRKQAESQIAELQVKLAE 1314  
 QY 49 IDTLRDTLEER---NATVESIQNALNKAMLCSTLKKQMKFLQRODDETRKQAREEAHR- 103  
 DB 1315 IERRASELQEKCTKLOQEAENITNQLAEALKASAAVKSASNMESQLTEAQQLLEETRQ 1374  
 QY 104 ---LCKMKMTMEQTEILLQSORSEVEEMIRDMVGQSAVQLAVYCVSLKKEYENLKEAR 160  
 DB 1375 KLGLSSKLRQIESKEKALQQLDEEDDAKRN---ERKLAEVTTQMOEIKKKAEDADLA 1431  
 QY 161 KATGELADRLKDLVSSRSKTKTL--NTELDQAKLELRSQKD---LOSADQETSLR 213  
 DB 1432 KELEEGKRRINKDIEALERQVKELIAONDRIDKSKKKIQSELEDATIELEQRKTVLE 1491  
 QY 214 KK 215  
 DB 1492 KK 1493

RESULT 21  
 Q9M0W8 PRELIMINARY; PRT; 2056 AA.  
 AC Q9M0W8; 01-MAY-2000 (TREMBlrel. 13, Created)  
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE ZIP PROTEIN  
 GN ZIP OR CG15792.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Braachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 RN  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BERKELEY;  
 RX MEDLINE-20196006; PubMed-10731132;  
 RA Adams M.D., Cealniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
 RA Abril J.F., Aghayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
 RA Ballew R.M., Basu A., Bayendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolintsov S.,  
 RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,  
 RA Burris K.C., Busam D.A., Butler H., Cadien E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.C., Dunn P.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dun P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Glodde A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegyam C.,  
 RA Jalali M., Kalush E., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Matei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Mostreli A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleby J.M.,  
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weisenbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yen R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of Drosophila melanogaster";  
 RL Science 287:2185-2195(2000).  
 DR EMBL; AF003465; AAF47311.1; -.  
 DR HSSP; P10587; 1BR2.  
 DR FlyBase; FBgn0005634; zip.  
 DR InterPro; IPR000048; IQ.  
 DR InterPro; IPR001609; myosin\_head.  
 DR InterPro; IPR004009; Myosin\_N.  
 DR InterPro; IPR002928; Myosin\_tail.  
 DR Pfam; PF00612; IQ; 1.  
 DR Pfam; PF0063; myosin\_head; 2.  
 DR Pfam; PF02736; Myosin\_N; 1.  
 DR Pfam; PF01576; Myosin\_tail; 1.  
 DR PRINTS; PR00193; MYOSINHEAVY  
 DR ProDom; PD000355; myosin\_head; 1.  
 DR SMART; SM00015; IQ; 1.  
 DR SMART; SM00242; MYSC; 1.  
 DR PROSITE; PSS0096; IQ; 1.  
 SQ SEQUENCE 2056 AA; 236627 MW; 1D074D9CCE1538E4 CRC64;

Query Match 15.4%; Score 166; DB 5; Length 2056;  
 Best Local Similarity 25.2%; Pred. No. 0.17;  
 Matches 61; Conservative 47; Mismatches 96; Indels 38; Gaps 8;

QY 1 KTIINKLFFDLQAEENVDAE--FLKNELDSYKAQLSQDKREKRSQ-----AI 48  
 DB 1302 KTVLEK-----AKGTLEENADLATELRVSVSSRQENDRRKQAESQIAELQVKLAE 1353  
 QY 49 IDTLRDTLEER---NATVESIQNALNKAMLCSTLKKQMKFLQRODDETRKQAREEAHR- 103  
 DB 1354 IERRASELQEKCTKLOQEAENITNQLAEALKASAAVKSASNMESQLTEAQQLLEETRQ 1413  
 QY 104 ---LCKMKMTMEQTEILLQSORSEVEEMIRDMVGQSAVQLAVYCVSLKKEYENLKEAR 160  
 DB 1414 KLGLSSKLRQIESKEKALQQLDEEDDAKRN---ERKLAEVTTQMOEIKKKAEDADLA 1470  
 QY 161 KATGELADRLKDLVSSRSKTKTL--NTELDQAKLELRSQKD---LOSADQETSLR 213  
 DB 1471 KELEEGKRRINKDIEALERQVKELIAONDRIDKSKKKIQSELEDATIELEQRKTVLE 1550  
 QY 214 KK 215  
 DB 1531 KK 1532

RESULT 22  
 Q94987 PRELIMINARY; PRT; 2057 AA.  
 AC Q94987; 01-FEB-1997 (TREMBlrel. 02, Created)  
 DT 01-FEB-1997 (TREMBlrel. 02, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE NONMUSCLE MYOSIN-II HEAVY CHAIN.

GN ZIP OR CG15792.  
OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_TaxID=1227;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=96144835; PubMed=8568878;  
RA Mansfield S.G., al-Shirawi D.Y., Ketchum A.S., Newbern E.C.,  
RA Kiehart D.P.,  
RT "Molecular organization and alternative splicing in zipper, the gene  
that encodes the Drosophila non-muscle myosin II heavy chain."  
RL J. Mol. Biol. 255:98-109(1996).  
DR EMBL: U35816; AAB09049.1; -  
DR EMBL: U35816; AAB09050.1; -  
DR HSSP: P10587; 1BR2.  
DR FLYBase; FBgn0005634; zip.  
DR InterPro: IPR000048; IO.  
DR InterPro: IPR001609; myosin\_head.  
DR InterPro: IPR004009; myosin\_N.  
DR InterPro: IPR002928; myosin\_tail.  
DR Pfam; PF00612; IO; 1.  
DR Pfam; PF00063; myosin\_head; 2.  
DR Pfam; PF02736; Myosin\_N; 1.  
DR Pfam; PF01576; Myosin\_tail; 1.  
DR PRINTS; PRO0193; MYOSINHEAVY.  
DR ProDom; PD000355; myosin\_head; 1.  
DR SMART; SM00015; IO; 1.  
DR SMART; SM00242; MYSC; 1.  
DR PROSITE; PS50096; IO; 1.  
SQ SEQUENCE 2057 AA; 236642 MW; 0D59519C1E83A411 CRC64;

Query Match 15.4%; Score 166; DB 5; Length 2057;  
Best Local Similarity 23.2%; Pred. No. 0.17;  
Matches 61; Conservative 47; Mismatches 96; Indels 38; Gaps 8;

QY 1 KTIINKLFFDLAEEENVLDAE--FLKNELDVKAQLSOKREKRDSQ-----AI 48  
DB 1303 KTVLEK-----AKGLEENADLATELRSVSSRRDNRKKAQSAELQVKLAE 1354  
QY 49 IDLRLDTLEER---NATVESLONLNKAKMLCSTLKKQMKFLRQRODETKQAREEHR- 103  
DB 1355 IERARSELQEKCKTKLQGEANITNQLFEAEIKASAAVNASMESQLTEAQQLLEERQ 1414  
QY 104 ---LKCCKMTMEQLELLQSRSEVEEMIRDMGVGQSAVEQLAVYCVSLKREYENLKEAR 160  
DB 1415 KLGISSKLRQIESEKEALQEQLEEDDEKRRNY---ERKLAETVTQOMQEKKKAEDADLA 1471  
QY 161 KATGELADRLKKDLVSSRSKLT---NTELDQAKLELRSQKD---LQSADEITSLR 213  
DB 1472 KELEGGKKRLKNDIEALERQVKELIAQNDRLDKSKKTIQSELEDAITLEAQRTKVLLE 1531  
QY 214 KK 215  
DB 1532 KK 1533  
RESULT 23  
Q90YT2  
ID Q90YT2 PRELIMINARY; PRT; 1447 AA.  
AC Q90YT2;  
DT 01-MAY-2000 (Tremblrel. 13, Created)  
DT 01-OCT-2001 (Tremblrel. 18, last sequence update)  
DT 01-OCT-2001 (Tremblrel. 18, last annotation update)  
DE MEA2/GOLGA3 PROTEIN.  
GN MEA2/GOLGA3.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]

RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL6;  
RA Matsukuma S.;  
RT "Mea2/Golga3 Gene Product is Indispensable for Spermatogenesis in the  
Mouse."  
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AB029537; BAA66890.2; JOINED.  
DR EMBL: AB029521; BAA66890.2; JOINED.  
DR EMBL: AB029522; BAA66890.2; JOINED.  
DR EMBL: AB029523; BAA66890.2; JOINED.  
DR EMBL: AB029524; BAA66890.2; JOINED.  
DR EMBL: AB029525; BAA66890.2; JOINED.  
DR EMBL: AB029526; BAA66890.2; JOINED.  
DR EMBL: AB029527; BAA66890.2; JOINED.  
DR EMBL: AB029528; BAA66890.2; JOINED.  
DR EMBL: AB029529; BAA66890.2; JOINED.  
DR EMBL: AB029530; BAA66890.2; JOINED.  
DR EMBL: AB029531; BAA66890.2; JOINED.  
DR EMBL: AB029532; BAA66890.2; JOINED.  
DR EMBL: AB029533; BAA66890.2; JOINED.  
DR EMBL: AB029534; BAA66890.2; JOINED.  
DR EMBL: AB029535; BAA66890.2; JOINED.  
DR EMBL: AB029536; BAA66890.2; JOINED.  
SQ SEQUENCE 1447 AA; 162776 MW; 53087BE7460B3E6F CRC64;

Query Match 15.4%; Score 165.5; DB 11; Length 1447;  
Best Local Similarity 24.1%; Pred. No. 0.13;  
Matches 70; Conservative 47; Mismatches 86; Indels 87; Gaps 12;

QY 10 DLAOEEENVLDA--EFLKNE-----LDSVKAQLSOKREKR-----DSQAIITDLRD 54  
DB 712 ELQREADSRDEDAIHFLQKEKIVLEVALQSAKSDKEELDRGARLRLEDTEESGLLEQLRQ 771  
QY 55 TLEERNATVESLONLNKAKMLCSTLKKQ--KFLBQ-----RODET-----KQ 96  
DB 772 DLAVKSNQVEHLOOE-----TATLRKQOKQVQEPVLQKRVNVEYRRDATSRDQLINE 824  
QY 97 AREEAHRLKCKMKMTMEQLELLQSRSEVE---EMIRDMGVGSAVEQLAVYCVSLKKE 152  
DB 825 LKATKKRLDSEMKELRQELIKQGEKTVVEHSLQDKMSLVHQQMKELGHLQSVQKE 884  
QY 153 YEN-----LKEA---RKATGELADRLKKDLVSSRSKLTNLTLELDOA 191  
DB 885 RDEMEIHQLSPDKQEQIALTEANETLKQIEELQQAKKAIETQKKMKRLSDLSLA 944  
QY 192 KLELRSAQKDLQSA-----DQETISLRK---SDP 219  
DB 945 QKEKTKHKAVERNVSILSRRLQALASKAETDAELNQLRAQSTGSSSDP 994  
RESULT 24  
Q90YT3  
ID Q90YT3 PRELIMINARY; PRT; 1487 AA.  
AC Q90YT3;  
DT 01-MAY-2000 (Tremblrel. 13, Created)  
DT 01-OCT-2001 (Tremblrel. 18, last sequence update)  
DT 01-DEC-2001 (Tremblrel. 19, last annotation update)  
DE MALE ENHANCED ANTIGEN 2/GOLGI AUTOANTIGEN, GOLGIN SUBFAMILY A, 3.  
GN MEA2/GOLGA3.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL6;  
RA Matsukuma S.;  
RT "Mea2/Golga3 Gene Product is Indispensable for Spermatogenesis in the  
Mouse."  
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AB029537; BAA66889.2; JOINED.  
DR EMBL: AB029521; BAA66889.2; JOINED.



Best Local Similarity 20.9%; Pred. No. 0.17;  
Matches 49; Conservative 61; Mismatches 90; Indels 34; Gaps 6;

OY 5 NKLFDLAQEEENVLDL-----FLKNELDYSKALDSOKDRKRSQAIIIDL 53  
DB 676 NDLFQIQLTQEDSLDADEEKYSKVLQKADMEGRILELDQSEENSATTLLEAKKLN 735  
OY 54 DTLERNATVESLONALKKAEMLSTLKKOMFLERODETKQAREEAHRLCKKMTQO 113  
DB 726 GEIEFLKDKDVESLESSIQKAEQEKAKDQIKTL--NDNNREKEQITTKMQEKKADE 792  
OY 114 IELLQSORSEVEEMIRDMGQSAVEQLAVYCVSLKREYENL-----KEARKA 162  
DB 793 LQKTEESLRAEEEEKVSNLKKAKALEQ-----AVDEMEENLSREQKVRADVEKARKV 846  
OY 163 TGEIADRLKDLVSRSLKT--LNTPELDQAKLELSAQKDSAQDQETLSLRK 215  
DB 847 EGEL--KQNEMLNDLERNKSELERQLRKKEMLGANSKLTEDENNIVATLQRK 898

RESULT 27  
026079  
ID 026079 PRELIMINARY; PRT: 1941 AA.  
AC 026079;  
DT 01-NOV-1996 (Tremblrel. 01, Created)  
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)  
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)  
DE MYOSIN HEAVY CHAIN.  
OS Placopecten magellanicus (Sea scallop).  
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Pectinoidea;  
OC Pectinoidea; Pectinidae; Placopecten.  
OX NCBI\_TaxID=6577;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=SKETALE MUSCLE;  
RA Perreault-Micale C., Kalabokis V., Nyitrai L., Szent-Gyorgyi A.G.;  
RT "Sequence variations in the surface loop near the nucleotide binding  
site modulate the ATP turnover rates of molluscan myosins.";  
RL J. Muscle Res. Cell Motil. 0:0-0(1996).  
DR EMBL: U59294; AAB03660.1; -;  
DR HSSP: P24733; IWDC.  
DR InterPro: IPR000048; IQ.  
DR InterPro: IPR001609; myosin\_head.  
DR InterPro: IPR004009; myosin\_N.  
DR InterPro: IPR002928; myosin\_tail.  
DR InterPro: IPR002017; Spectrin.  
DR Pfam: PF00612; IQ; 2.  
DR Pfam: PF00063; myosin\_head; 1.  
DR Pfam: PF02736; Myosin\_N; 1.  
DR Pfam: PF01576; Myosin\_tail; 1.  
DR PRINTS: PR00193; MYOSINHEAVY.  
DR PRODOM: PD000355; myosin\_head; 1.  
DR SMART: SM00015; IQ; 1.  
DR SMART: SM00242; MYSC; 1.  
DR PROSITE: PSS0096; IQ; 1.  
SQ SEQUENCE 1941 AA; 223243 MW; E2AD1637FFDB8127 CRC64;

Query Match 15.3%; Score 165; DB 5; Length 1941;  
Best Local Similarity 24.2%; Pred. No. 0.19;  
Matches 72; Conservative 52; Mismatches 88; Indels 86; Gaps 12;

OY 1 KTIINKLFFD--LQOEENVLDAEFLKNELDLVS-----AQLSQK 38  
DB 907 KLIMQKADFESQIKELERLDEEDDASDLGKIKKMEGDNANLKKDIGELHSLQSEQ 966  
OY 39 DREKRDQAIIIDL-----RDTLEERN-ATVESLQ-----NALNKA 74  
DB 967 EKAKHDNQ--ISTLQSGMSQODEHIKLNKKEKALAEANKKTSLSLQAEKCHLNK-- 1022  
OY 75 MLCSTLKKOMFLERODETKQAREEAHRLCKKMK-----TMEQIELLQSORSEVEEMI 129  
DB 1023 -LKAKLEQALDELNDLERNERKKVGDVEKAKSVQDLKSTQENVEDLERVKR-ELLEENV 1080

OY 130 R-----DMVGQSAVEQLAVYCVSLKREYENLKEARKATGELADRLKDLVSSR 178  
DB 1081 RRKEAEITTLNSKLEDEQNVLVSQLRKIKELQARIEELFEELERNAKRSVEEQRAELN 1140  
OY 179 SKLTLNTELDQA-----KLELRSQKDLQSA---DQETLSLRKSSD 218  
DB 1141 RELEELERLDEAGATSAQIELNKKREAEILLKIRPDLFASLQHEAQISAIRKKHOD 1198

RESULT 28  
026080  
ID 026080 PRELIMINARY; PRT: 1950 AA.  
AC 026080;  
DT 01-NOV-1996 (Tremblrel. 01, Created)  
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)  
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)  
DE MYOSIN HEAVY CHAIN.  
OS Placopecten magellanicus (Sea scallop).  
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Pectinoidea;  
OC Pectinoidea; Pectinidae; Placopecten.  
OX NCBI\_TaxID=6577;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=ADDUCTOR MUSCLE;  
RA Perreault-Micale C., Kalabokis V., Nyitrai L., Szent-Gyorgyi A.G.;  
RT "Sequence variations in the surface loop near the nucleotide binding  
site modulate the ATP turnover rates of molluscan myosins.";  
RL J. Muscle Res. Cell Motil. 0:0-0(1996).  
DR EMBL: U59295; AAB03661.1; -;  
DR HSSP: P24733; IWDC.  
DR InterPro: IPR000048; IQ.  
DR InterPro: IPR001609; myosin\_head.  
DR InterPro: IPR004009; myosin\_N.  
DR InterPro: IPR002928; myosin\_tail.  
DR InterPro: IPR002017; Spectrin.  
DR Pfam: PF00612; IQ; 2.  
DR Pfam: PF00063; myosin\_head; 1.  
DR Pfam: PF02736; Myosin\_N; 1.  
DR Pfam: PF01576; Myosin\_tail; 1.  
DR PRINTS: PR00193; MYOSINHEAVY.  
DR PRODOM: PD000355; myosin\_head; 1.  
DR SMART: SM00015; IQ; 1.  
DR SMART: SM00242; MYSC; 1.  
DR PROSITE: PSS0096; IQ; 1.  
SQ SEQUENCE 1950 AA; 224184 MW; 6FE358802352C19A CRC64;

Query Match 15.3%; Score 165; DB 5; Length 1950;  
Best Local Similarity 24.2%; Pred. No. 0.19;  
Matches 72; Conservative 52; Mismatches 88; Indels 86; Gaps 12;

OY 1 KTIINKLFFD--LQOEENVLDAEFLKNELDLVS-----AQLSQK 38  
DB 906 KLIMQKADFESQIKELERLDEEDDASDLGKIKKMEGDNANLKKDIGELHSLQSEQ 965  
OY 39 DREKRDQAIIIDL-----RDTLEERN-ATVESLQ-----NALNKA 74  
DB 966 EKAKHDNQ--ISTLQSGMSQODEHIKLNKKEKALAEANKKTSLSLQAEKCHLNK-- 1021  
OY 75 MLCSTLKKOMFLERODETKQAREEAHRLCKKMK-----TMEQIELLQSORSEVEEMI 129  
DB 1022 -LKAKLEQALDELNDLERNERKKVGDVEKAKSVQDLKSTQENVEDLERVKR-ELLEENV 1079  
OY 130 R-----DMVGQSAVEQLAVYCVSLKREYENLKEARKATGELADRLKDLVSSR 178  
DB 1080 RRKEAEITTLNSKLEDEQNVLVSQLRKIKELQARIEELFEELERNAKRSVEEQRAELN 1139  
OY 179 SKLTLNTELDQA-----KLELRSQKDLQSA---DQETLSLRKSSD 218  
DB 1140 RELEELERLDEAGATSAQIELNKKREAEILLKIRPDLFASLQHEAQISAIRKKHOD 1197

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RESULT 29
ID 025561 PRELIMINARY; PRT; 746 AA.
AC 025561;
DT 01-NOV-1996 (TEMBLrel. 01, Created)
DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TEMBLrel. 19, Last annotation update)
DE MYOSIN II HEAVY CHAIN (FRAGMENT).
OS Naegleria fowleri.
OC Eukaryota; Heterolobosea; Schizopyrenida; Vahlkampfiidae; Naegleria.
OX NCBI_TaxID=5763;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LEE MP;
RA Shaw D.R., Sullivan P.K., Marciano-Cabral F., Ennis H.L.;
RT "Codon usage in Naegleria fowleri."
RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; U04192; AAB01786.1; -.
DR InterPro: IPR002017; Spectrin.
FT NON_TER
SQ SEQUENCE 746 AA: 87781 MW: 3771A80AFC2FF43 CRC64;

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Query Match 15.3%; Score 164.5; DB 5; Length 746;
Best Local Similarity 22.7%; Pred. No. 0.083;
Matches 57; Conservative 57; Mismatches 104; Indels 33; Gaps 4;

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OY 1 KTIINKLFFDLAEEENVLDAEFLKNELDVSKAQLSOKDKREKRSQALIDTLRDTLEERN 60
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 167 KOLONELONETNLQKKSENERLQRELEKRELSLSDKQKSVLSLEKIRELT 226
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
OY 61 ATVESLONALKKAMELSTLKQMKFLEORODETKQA-REEAHLKCKMKTMEQIELLQ 119
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 227 ALLETBESSKTDLDKRSKSKADKEVKRLAQQLQETQALKEGTQCKKNADNRVKKLESELQ 286
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
OY 120 SQRSSEVEEMIRDMG-----VQSAVEQLAVYCVSLKKEVENLKEARKATGE 165
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 287 GVKSEERDLNLDNNTSGDMNGLKQLDESNNLVAKLKAELQKQLKSLDHDHGDREPEEE 346
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
OY 166 LADLKLKLDVSSRSKL-----KTLTELDQAKLELRSAQKDLQSDA---Q 207
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 347 QLDLRLKROLQELTSLSDANOKTQQAASRLNLESENRLKSEVSRLEDLQENRRLKQ 406
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
OY 208 EITSLRKSSD 218
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 407 EMERVQSESEV 417

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FT VARIANT 6 6 W -> *.
SQ SEQUENCE 2501 AA: 286525 MW: F3E087071B771F62 CRC64;

Query Match 15.3%; Score 164.5; DB 5; Length 2501;
Best Local Similarity 24.3%; Pred. No. 0.25;
Matches 66; Conservative 52; Mismatches 93; Indels 61; Gaps 11;

OY 1 KTII-----KLFPLDAEEENVLDAEFLKNELDVSKAQLSOKD-----REK 42
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 1243 KSVLEAQTKLSDLDQREKESAQQLVDNLKVELDKERKELAQVSAFEAQTKLSDLDQRL 1302
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
OY 43 RDSQAIDTLRDTLEER-----NATVES-----LONALKKAMELSTLK-----KOM 84
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 1303 ESAQQLVDNLKVELDKERKELAKVNSAFEAQTKLSDLDQLEKDLAQQLVDTLKVELDKEK 1362
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
OY 85 KFLQ-----RODETKQAREEAHLKCKMKT-----MEQIELLOSQRSEVE 136
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 1363 KELAQVNSPEAQTKLSDLDQRLKESAQQLVDNLKVELDKERKELAQVKSVEIAEQTKLSD 1422
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
OY 127 EMTRDMGVGSNAEQVLAVYCVSLKKEVENLKEARKATGELADRLKDLVSSRSKTLTNT 186
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 1423 DLQOKESAQQLVDNL-----MELDKERKELAQVKSALG-AQTKLSDLEQOKESVQDL-- 1476
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
OY 187 ELDOAKLELRSAQKDLQSDAEOETSLRKSSD 218
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 1477 -VDNLKVELDKERKELAKVNSAFEAQTKLSD 1507

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RESULT 31
ID 09UT73 PRELIMINARY; PRT; 1940 AA.
AC 09UT73;
DT 01-MAY-2000 (TEMBLrel. 13, Created)
DT 01-MAY-2000 (TEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TEMBLrel. 19, Last annotation update)
DE MYOSIN HEAVY CHAIN.
OS Pecten maximus (King scallop) (Pilgrim's clam).
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Pectinoidea;
OC Pectinoidea; Pectinidae; Pecten.
OX NCBI_TaxID=6579;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=ADDUCTOR MUSCLE;
RA Jones D.P., Patel H., Chantler P.D.;
RT "Primary structure of myosin from the striated adductor muscle of the
   Atlantic scallop, Pecten maximus."
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF134172; AAD52842.1; -.
DR HSSP; P24733; IWDG.
DR InterPro: IPR000048; IQ.
DR InterPro: IPR001609; myosin_head.
DR InterPro: IPR004009; Myosin_N.
DR InterPro: IPR002928; Myosin_tail.
DR InterPro: IPR002017; Spectrin.
DR Pfam; PF00612; IQ; 2.
DR Pfam; PF00063; myosin_head; 1.
DR Pfam; PF02736; Myosin_N; 1.
DR Pfam; PF01576; Myosin_tail; 1.
DR PRINTS; PR00193; MYOSINHEAVY.
DR ProDom; PD000355; myosin_head; 1.
DR SMART; SM00015; IQ; 1.
DR SMART; SM00242; MYSC; 1.
DR PROSITE; PS50096; IQ; 1.
SQ SEQUENCE 1940 AA: 223141 MW: A3D09DECBEB16F90 CRC64;

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Query Match 15.3%; Score 164; DB 5; Length 1940;
Best Local Similarity 24.8%; Pred. No. 0.21;
Matches 74; Conservative 49; Mismatches 89; Indels 86; Gaps 12;

OY 1 KTIINKLFFD-LAQEEENVLDAEFLKNELDVSK-----AQLSQK 38
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

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Dh 907 KLINOKADEFSOIKLEBERLLDEEDAAADLEGIKKMETDONSNIKKDIDGLENLTQKAEQ 966  
Qy 39 DREKRSQAIDTL-----RDLEERN-ATVESIQ-----NALNKAE 74  
Dh 967 DKARKDNG-ISTOGEMAODDEHIGKLNKKKALEFNKNTSISLQAEKCHLNK-- 1022  
Qy 75 MLCSTLKKOMKFLPORODETKOAREHRLCKMK-----TMEQIELLOSORSEVEEMI 129  
Dh 1023 -LKAKLEQALDELNDLNEREKVGDVEKARKRVEQDKSTQEWVEDLEVRK- ELEENV 1080  
Qy 130 R-----DMGVGSAVEOLAVCVSLKKEYENLKEARKKATGELADRLKLDVSSR 178  
Dh 1081 RRRKAEISTLNSKLEDEQNLVSOQRKVKELQARIEELEERNAARAKVEQRAELN 1140  
Qy 179 SKLTNTLTELDOA-----KLEIRSAQKDOSA-----DOEITSLRKSSD 218  
Dh 1141 RELEBERGERUDEAGAGTSAQTEILNKKRREALLKTRDLEASISQHEAQISLRRKHOD 1198  
RESULT 32  
Q9XIP6 PRELIMINARY; PRT; 1313 AA.  
AC 09XIP6:  
DT 01-NOV-1999 (TREMBlrel. 12, Created)  
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)  
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
DE F13011.30 PROTEIN.  
GN F13011.30.  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots; Rosidae;  
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.  
OX NCBI\_TaxID=3702;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA STRAIN=CV. COLUMBIA;  
RA Federspiel N.A., Palm C.J., Conway A.B., Conn L., Hansen N.F.,  
RA Altairi H., Araujo R., Huizar I., Rowley D., Buehler E., Dunn P.,  
RA Gonzalez A., Kremetskaia I., Kim C., Lenz C., Li J., Liu S.,  
RA Luros S., Schwartz J., Shinn P., Toriumi M., Vysotskaia V.S.,  
RA Walker M., Yu G., Ecker J., Theologis A., Davis R.W.,  
RA Submitted (May-2000) to the EMBL/GenBank/DBJ databases.  
RL EMBL: AC006193; AAD38273.1;  
DR EMBL: 1313 AA; 149137 MW; DBE383C4960F60C CRC64;  
SQ SEQUENCE 1313 AA; 149137 MW; DBE383C4960F60C CRC64;

Query Match 15.28; Score 163; DB 10; Length 1313;  
Best Local Similarity 22.88; Pred. NO. 0.17; Mismatches 81; Indels 94; Gaps 9;  
Matches 67; Conservative 52; Mismatches 81; Indels 94; Gaps 9;  
Qy 12 AOEENVLDD-----AEFLKNELDSVKAOL-SQDKREKDSQAIDTLRLDLEERNATVES 65  
Dh 182 AEATKTAIEIAEKAELIASLGLKALLSKKEKEKAEIGCEIYSKLK-----SEEL 234  
Qy 66 LQNLNKAEMICSTLKKOMKFLPORODETKOAR-----EEA 101  
Dh 235 LRGLERVYSILSESLKDEGLVQLKVDLEAKMAESCTNSVEEMKNKVHELEKEVES 294  
Qy 102 HRLCK-----MKTM-----EOIELL-----LOSOREVEEMIRDM 132  
Dh 295 NRSSSASSESSESVMKQALAEINHVLEHTKSDNAAQKEITELLETKEQRTDLEEGYGV 354  
Qy 133 GVGSAVEOLAVCVSLKKEYE-----NLKEARKATGELAD----- 168  
Dh 355 CIAKEEASKLENLVESIKSELSIQEKEKTRALDNEKKAATSIQNLQRTLESTELERCK 414  
Qy 169 -----RLKKDLVSSRSKLTTLTELDOAKLEIRSAQKDLSAQDOEITSLRKSSD 218  
Dh 415 VEEERKSKDMESTLALQEAESTESSEKATLVQOEELKNCSQVDSIKLASKE 468  
RESULT 33  
Q07380

ID 007380 PRELIMINARY; PRT; 1790 AA.  
AC 007380: P89692;  
DT 01-NOV-1996 (TREMBlrel. 01, Created)  
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)  
DE HYPOTHETICAL 206.5 KDA PROTEIN YDLO58W.  
GN US01 OR YDLO58W.  
OS Saccharomyces cerevisiae (Baker's yeast).  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.  
OX NCBI\_TaxID=4932;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Bloecker H., Brandt P.;  
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.  
DR EMBL: 274106; CAA98621.1; -;  
DR EMBL: 274105; CAA98620.1; -;  
DR SGD: 50002216; US01.  
DR InterPro: IPR002017; Spectrin.  
SQ SEQUENCE 1790 AA; 206450 MW; 90062544F55A52EE CRC64;

Query Match 15.28; Score 163; DB 3; Length 1790;  
Best Local Similarity 23.78; Pred. NO. 0.22; Mismatches 77; Indels 30; Gaps 7;  
Matches 51; Conservative 57; Mismatches 77; Indels 30; Gaps 7;  
Qy 10 DLAOEENVLDAEFLKNELDSVKAOLSQDKREKDSQAIDTLRLDLEERNATVESIQNA 69  
Dh 1424 ELEEKONTIS--LQDEI-----LSYKDKITNDEKLSIENDKRD-----LESLEQ 1471  
Qy 70 LNKAEMLCSTLKKOMKFLPORODETKOAREHRLCKMKMTMEQIELLOSORSEVEEMI 129  
Dh 1472 LRAQESKAKVEBGLKLEESSEKKALEKSKEM-----MKKLESTIESNETELKSSM 1525  
Qy 130 RDMGVGSAVEOLAVCVSLKKEYENLKEARKATGELADRL-----KDLVSSRSKLT---T 183  
Dh 1526 ETIKSDSEKLEQ-----SKRSABEDIKNLOHEKSDLSIRINESEKDIELKSLRIEAK 1579  
Qy 184 LNTLEDOAKLEIRSAQKDLSAQDOEITSLRKSSD 218  
Dh 1580 SGSELETYVQELNNAQEKIRINAENVTLSKLED 1614

RESULT 34  
Q06720 PRELIMINARY; PRT; 692 AA.  
AC 096720:  
DT 01-DEC-2001 (TREMBlrel. 19, Created)  
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
DE PARAMYOSIN-LIKE ALDERGEN (FRAGMENT).  
OS Dermatophagoides farinae (House-dust mite).  
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;  
OC Acariformes; Sarcoptiformes; Astigmata; Analgoidea; Pyroglyphidae;  
OC Dermatophagoides.  
OX NCBI\_TaxID=6954;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98389068; PubMed=9723675;  
RA Tsai L.C., Chao P.L., Shen H.D., Tang R.B., Chang T.C., Chang Z.N.,  
RA Hung M.W., Lee B.L., Chua K.Y.;  
RT "Isolation and characterization of a novel 98-kd Dermatophagoides  
RT farinae mite allergen."  
RL J. Allergy Clin. Immunol. 102:295-303(1998).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20062524; PubMed=10594536;  
RA Tsai L., Sun Y., Chao P., Ng H., Hung M., Hsieh K., Liaw S., Chua K.;  
RT "Sequence analysis and expression of a cDNA clone encoding a 98-kDa  
RT allergen in Dermatophagoides farinae."  
RL Clin. Exp. Allergy 29:1606-1613(1999).  
RN [3]  
RP SEQUENCE FROM N.A.

RA Tsai L.-C., Chao P.-L., Ng H.-P., Chua K.-Y.;  
 RL Submitted (FEb-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF552244; AAK39511.1; -  
 FT NON\_TER 692 692  
 SQ SEQUENCE 692 AA; 81372 MW; 61FC6380C9D7C9E2 CRC64;

Query Match 15.1%; Score 162; DB 5; Length 692;  
 Best Local Similarity 24.9%; Pred. No. 0.11; Indels 54; Gaps 10;  
 Matches 62; Conservative 54; Mismatches 79; Indels 54; Gaps 10;

QY 11 LAOEE-----ENVLDAEFLKNEIDSVKAQLSQK-----DRE-----KRDQ 46  
 Db 157 LEEERRRASEN--HAHTLEVELESILKYQDESEARLELERLUTKANGDAASKRYE 214  
 QY 47 AITLDTLEERNATV-----ESLQNALNKAEMLCSTLKQKMFLEQRD-----ET 94  
 Db 215 AELQAHADVEEELRRKKAOKISEVEEQLLEALINK-----CSLEKOKSRLOSEVEVLIMDL 270  
 QY 95 KOAREEAHRLCKMKTMEQTEILLQSORSEVEEMIRMGVQSAVEQLAVYCVSLK-- 151  
 Db 271 EKATRHAAQLEKRVAAQLEKINLDKNLEVTLM-----EQAKELRYKIAELQKQH 324  
 QY 152 EYENLKEARKATGELADRLKKDLVSSRSKLTTELDQAKLE---LRSQKDLQSDOE 208  
 Db 325 EYELRQGRQDLARENKKLDDDLAFAKSQDLANDAHRIHQEIEIKLENERDELAAVKE 384  
 QY 209 ITSRLKSD 217  
 Db 385 AETLRKOE 393

RESULT 35  
 QY9YHD5 PRELIMINARY; PRT; 826 AA.  
 ID QY9YHD5  
 AC QY9YHD5;  
 DT 01-MAY-1999 (TEMBLrel. 10, Created)  
 DT 01-MAY-1999 (TEMBLrel. 10, Last sequence update)  
 DT 01-DEC-2001 (TEMBLrel. 19, Last annotation update)  
 DE MYOSIN HEAVY CHAIN (FRAGMENT).  
 GN MHC-4.  
 OS Rana catesbeiana (Bull frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.  
 OX NCBI\_TaxID=8400;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=TAIL MUSCLE; HINDIII MUSCLE;  
 RA Hu H., Merrifield P., Atkinson B.G.;  
 RT "Expression of the Myosin Heavy Chain Genes in the Tail Muscle of  
 RT Thyroid Hormone-induced Metamorphosing Rana catesbeiana Tadpoles";  
 RL Dev. Genet. 0:0-0(1999).  
 DR EMBL: AF097907; AAD13772.1; -  
 DR InterPro: IPR002928; Myosin\_tail.  
 DR InterPro: IPR000533; Tropomyosin.  
 DR Pfam: PF01576; Myosin\_tail; 1.  
 DR PRINTS: PR00194; TROPOMYOSIN.  
 FT NON\_TER 1  
 FT SEQUENCE 826 AA; 95362 MW; 8F9E3B0579D0F483 CRC64;

Query Match 15.1%; Score 162; DB 13; Length 826;  
 Best Local Similarity 23.4%; Pred. No. 0.12; Indels 94; Gaps 12;  
 Matches 66; Conservative 49; Mismatches 79; Indels 94; Gaps 12;  
 QY 11 LAOEEENVLDAEFLKNEIDS--VKAQLSQKRE---KRDQAIDTLTLE---ERNA 61  
 Db 442 LEHEEARILRVQLNLNKKSEVDKRIAEKDEENQKRNQRAIDTQSTLDSLEIRSD 501  
 QY 62 TV---ESLQNALNKAEMLC-----TLKKQ 83  
 Db 502 ALRLKKMEGDLNLELQIOLSHANROASEAKQLRNVOQLKDAQLHLDDALRGEDLKEQ 561

QY 84 MKFLEQR-----QDETQKAREAHRLCKMKTMEQTEILLQSOR----- 122  
 Db 562 VAVIERRNNNQALIEIESRSRLTEQTERSRLAE--ELLDASERQLHSONTILNSKK 620  
 QY 123 -----SEVEEMIRDM---GVGQSAVEQLAVYCVSLKREYENLKEARKATGELADR 169  
 Db 621 LESDIAQLTNEVEESVQESRNAEDKAKKAITDALMAELKEKED-----TSAHLR 672  
 QY 170 LKRLVSSRSKLTNTLQDA--KLELRSAQKDLQSDQDETSLRKSSD 218  
 Db 673 MKKNLEOS---VKDLQHRLEDAEQLAMKGGKQLOKLEVRLESELDN 719

RESULT 36  
 QY9NJ23 PRELIMINARY; PRT; 1219 AA.  
 ID QY9NJ23  
 AC QY9NJ23;  
 DT 01-OCT-2000 (TEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TEMBLrel. 15, Last sequence update)  
 DT 01-DEC-2001 (TEMBLrel. 19, Last annotation update)  
 DE MYOSIN HEAVY CHAIN STRIATED MUSCLE SPECIFIC ISOFORM (FRAGMENT).  
 GN MHC.  
 OS Aequipecten irradians (Bay scallop).  
 OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Pectinoida;  
 OC Pectinoidea; Pectinidae; Argopecten.  
 OX NCBI\_TaxID=31199;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20090924; pubmed=10623517;  
 RA Yamada A., Yoshio M., OIwa K., Nyitray L.;  
 RT "Catchin, a novel protein in molluscan catch muscles, is produced by  
 RT alternative splicing from the myosin heavy chain gene";  
 RL J. Mol. Biol. 285:169-178(2000).  
 DR EMBL: AF183909; AAF62391.1; -  
 DR HSSP: P24733; IWDG.  
 DR InterPro: IPR000048; IQ.  
 DR InterPro: IPR001609; myosin\_head.  
 DR InterPro: IPR002928; Myosin\_tail.  
 DR InterPro: IPR002017; Spectrin.  
 DR InterPro: IPR000533; Tropomyosin.  
 DR Pfam: PF00612; IQ; 2.  
 DR Pfam: PF00063; myosin\_head; 1.  
 DR Pfam: PF01576; Myosin\_tail; 1.  
 DR PRINTS: PR00194; TROPOMYOSIN.  
 DR PRODOM: PD000355; myosin\_head; 1.  
 DR SMART: SM00015; IQ; 1.  
 DR PROSITE: PS50096; IQ; 1.  
 FT NON\_TER 1  
 FT SEQUENCE 1219 AA; 141202 MW; BAC6F574DA4AFBBB CRC64;

Query Match 15.1%; Score 162; DB 5; Length 1219;  
 Best Local Similarity 24.5%; Pred. No. 0.18; Indels 86; Gaps 12;  
 Matches 73; Conservative 50; Mismatches 89; Indels 86; Gaps 12;

QY 1 KTIINKLFFD-----LAOEEENVLDAEFLKNEIDSVKAQ-----SQK 38  
 Db 185 KLIMQKADFESQIKLELERLIDDEDAADLEGIKKKMEADVANKKDIGLENTLQRAEQ 244  
 QY 39 DREKRQAIDTL-----RDTLEERN--ATVESIQ-----NALNKA 74  
 Db 245 DKAHKDNO--ISTIQGLSODDEHIGKLNKKALEANKKTSLSLOAEKCHLNK-- 300  
 QY 75 MLCSTLKQKMFLEBORDETQKAREAHRLCKMK---TMEQTEILLQSORSEVEEMI 129  
 Db 301 -LKAQLQALDELBDNLERKKVGVDEKAKKVEQDLKSTQENVEDLERVKR--ELEBNV 358  
 QY 130 R-----DMGVQSAVEQLAVYCVSLKREYENLKEARKATGELADLKKDLYSSR 178  
 Db 359 RRKEAEISSLSKLEDRONLSQLRKIKELQARIIELEELAEARNARAVEKQRAELN 418  
 QY 179 SKLTMTLQDA-----KLELRSAQKDLQSA---DDETSLRKSSD 218

Db 419 RELEBELGERLDEAGAGSAQIETLNKKREAEELIKTRDLSEASLOHEAOISALRRKHOD 476

RESULT 37

09NJ22 PRELIMINARY: PRT; 1229 AA.

AC 09NJ22;

DT 01-OCT-2000 (TREMBlrel. 15, Created)

DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)

DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)

DE MYOSIN HEAVY CHAIN CATCH (SMOOTH) MUSCLE SPECIFIC ISOFORM (FRAGMENT).

GN MHC.

OS Aequipecten irradians (Bay scallop).

OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Pectinoidea; Pectinidae; Argopecten.

OX NCBI\_Taxid=31199;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=20090924; PubMed=10623517;

RA Yamada A., Yoshio M., Owa K., Nyitray L.;

RT "Catchin, a novel protein in molluscan catch muscles, is produced by alternative splicing from the myosin heavy chain gene.";

RL J. Mol. Biol. 295:169-178(2000).

DR EMBL: AF183909; AAF62392.1; .

DR HSSP: P24733; IMDC.

DR InterPro: IPR000048; IQ.

DR InterPro: IPR001609; myosin\_head.

DR InterPro: IPR002928; myosin\_tail.

DR InterPro: IPR002017; Spectrin.

DR InterPro: IPR000533; Tropomyosin.

DR Pfam: PF00063; myosin\_head.1.

DR Pfam: PF01576; myosin\_tail.1.

DR PRINTS: PR00194; TROPOMYOSIN.

DR PRODOM: PD000355; myosin\_head.1.

DR SMART: SM00015; IQ.1.

DR PROSITE: PS50096; IQ.1.

FT NON\_TER 1

SO SEQUENCE 1229 AA; 142180 MW; 1764276CB904FDC9 CRC64;

Query Match 15.1%; Score 162; DB 5; Length 1229;

Best Local Similarity 24.5%; Pred. No. 0.18;

Matches 73; Conservative 50; Mismatches 89; Indels 86; Gaps 12;

QY 1 KTIINKLFPD-----LAQEEENVLDAEFLKNELDVKAQL-----SOK 38

Db 185 KLIMQKADFEQIKELERLDEEDAAADLEGIKKMEADANLKKDIDGLDENTLQRAEQ 244

QY 39 DREKRDQAIIIDL-----RDTLEERN-ATVESLQ-----NALKAE 74

Db 245 DKAKHKNQ--ISTLQGEISQODEHIGLKNKKALEANKKTSLSLAEEKCHLKNK-- 300

QY 75 MLCSTLKKQKMFLEQRODETKQAREEAHRLKCKMK-----TMEQIELLLQSQRSEVEEMI 129

Db 301 -LKAKLQALDELNDNERKKVGDVEKAKRVEQDLKSTQENVEDLERVKR-ELBENV 358

QY 130 R-----DMGVGSAVEQLAVYCVSLKKEVENLKEARKATGELADLKLKDVSSR 178

Db 359 RRKAETISLSNLSKLEDEQNLVSQLOKRIKELQARIIELEELAEARNARAVEKQRAELN 418

QY 179 SKLKLNTLMDQA-----KLELRSQKDLQSA-----DOETSLRKSSD 218

Db 419 RELEBELGERLDEAGAGSAQIETLNKKREAEELIKTRDLSEASLOHEAOISALRRKHOD 476

RESULT 38

09NJ21 PRELIMINARY: PRT; 1243 AA.

AC 09NJ21;

DT 01-OCT-2000 (TREMBlrel. 15, Created)

DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)

DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)

DE MYOSIN HEAVY CHAIN CARDIAC MUSCLE SPECIFIC ISOFORM 1 (FRAGMENT).

GN MHC.

OS Aequipecten irradians (Bay scallop).

OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Pectinoidea; Pectinidae; Argopecten.

OX NCBI\_Taxid=31199;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=20090924; PubMed=10623517;

RA Yamada A., Yoshio M., Owa K., Nyitray L.;

RT "Catchin, a novel protein in molluscan catch muscles, is produced by alternative splicing from the myosin heavy chain gene.";

RL J. Mol. Biol. 295:169-178(2000).

DR EMBL: AF183909; AAF62394.1; .

DR HSSP: P24733; IMDC.

DR InterPro: IPR000048; IQ.

DR InterPro: IPR001609; myosin\_head.

DR InterPro: IPR002928; myosin\_tail.

DR InterPro: IPR002017; Spectrin.

DR InterPro: IPR000533; Tropomyosin.

DR Pfam: PF00063; myosin\_head.1.

DR Pfam: PF01576; myosin\_tail.1.

DR PRINTS: PR00194; TROPOMYOSIN.

DR PRODOM: PD000355; myosin\_head.1.

DR SMART: SM00015; IQ.1.

DR PROSITE: PS50096; IQ.1.

FT NON\_TER 1

SO SEQUENCE 1243 AA; 143531 MW; B5C7219BFF2B5E8AE CRC64;

Query Match 15.1%; Score 162; DB 5; Length 1243;

Best Local Similarity 24.5%; Pred. No. 0.18;

Matches 73; Conservative 50; Mismatches 89; Indels 86; Gaps 12;

QY 1 KTIINKLFPD-----LAQEEENVLDAEFLKNELDVKAQL-----SOK 38

Db 185 KLIMQKADFEQIKELERLDEEDAAADLEGIKKMEADANLKKDIDGLDENTLQRAEQ 244

QY 39 DREKRDQAIIIDL-----RDTLEERN-ATVESLQ-----NALKAE 74

Db 245 DKAKHKNQ--ISTLQGEISQODEHIGLKNKKALEANKKTSLSLAEEKCHLKNK-- 300

QY 75 MLCSTLKKQKMFLEQRODETKQAREEAHRLKCKMK-----TMEQIELLLQSQRSEVEEMI 129

Db 301 -LKAKLQALDELNDNERKKVGDVEKAKRVEQDLKSTQENVEDLERVKR-ELBENV 358

QY 130 R-----DMGVGSAVEQLAVYCVSLKKEVENLKEARKATGELADLKLKDVSSR 178

Db 359 RRKAETISLSNLSKLEDEQNLVSQLOKRIKELQARIIELEELAEARNARAVEKQRAELN 418

QY 179 SKLKLNTLMDQA-----KLELRSQKDLQSA-----DOETSLRKSSD 218

Db 419 RELEBELGERLDEAGAGSAQIETLNKKREAEELIKTRDLSEASLOHEAOISALRRKHOD 476

RESULT 39

09NJ20 PRELIMINARY: PRT; 1253 AA.

AC 09NJ20;

DT 01-OCT-2000 (TREMBlrel. 15, Created)

DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)

DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)

DE MYOSIN HEAVY CHAIN CARDIAC MUSCLE SPECIFIC ISOFORM 2 (FRAGMENT).

GN MHC.

OS Aequipecten irradians (Bay scallop).

OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Pectinoidea; Pectinidae; Argopecten.

OX NCBI\_Taxid=31199;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=20090924; PubMed=10623517;

RA Yamada A., Yoshio M., Owa K., Nyitray L.;

RT "Catchin, a novel protein in molluscan catch muscles, is produced by

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RT alternative splicing from the myosin heavy chain gene."
RL J. Mol. Biol. 295:169-178(2000).
DR EMBL: AF183909; AAF62395.1; -.
DR HSSP: P24733; 1WDC.
DR InterPro: IPR000048; IQ.
DR InterPro: IPR001609; myosin_head.
DR InterPro: IPR002928; Myosin_tail.
DR InterPro: IPR002017; Spectrin.
DR InterPro: IPR000533; Tropomyosin.
DR Pfam: PF00063; myosin_head; 1.
DR Pfam: PF01576; myosin_tail; 1.
DR PRINTS: PR00194; TROPOMYOSIN.
DR ProDom: PD000355; myosin_head; 1.
DR SMART: SM00015; IQ; 1.
DR PROSITE: PS50096; IQ; 1.
DR NON_TER 1
SQ SEQUENCE 1253 AA; 144774 MW; 56E4FF0226B58C92 CRC64;

Query Match 15.1%; Score 162; DB 5; Length 1253;
Best Local Similarity 24.5%; Pred. No. 0.18; Mismatches 89; Indels 86; Gaps 12;
Matches 73; Conservative 50;

QY 1 KTIINKLFFD-----LAQEEENVLDAEFLKNEIDSVKAQL-----SOK 38
DB 185 KLIMQKADFESEQIKELERLDEDAADLEGIKKMEADANLKDIDGDLNTLOKAEQ 244
QY 39 DREKRSQAIIIDL-----RDTLEERN-ATVESLO-----NALNKA 74
DB 245 DKAKKDNO--ISTLQGISQODEHIGKLNKKEKALEANKKTSLSLAEDKCNHLNK-- 300
QY 75 MLCSTLKKOMKFLERODETKQAREEAHRLCKMK-----TMEQIELLLQSORSEVEEMI 129
DB 301 -LKAKLEQALDELNDNEREKKVGDEYKAKRKVEQDLKSTQENVEDLERVKR-ELLEENV 358
QY 130 R-----DMVGQSAVEQLAVYCVSLKKEYENLKEARKATGELADRLKDLVSSR 178
DB 359 RRKEAEISLNSKLEEDONLVSQLQRIKELQARIEELEELAEARNARAVEQKORAEIN 418
QY 179 SKLTLNTELDQA-----KLELRSQOKDLSA-----DOETISLRKSSD 218
DB 419 RELEELGERLDEAGATSAQIELNKKRPAELIKIRDLLEASLOHEAOISALRRKHOD 476

RESULT 40
Q17042 PRELIMINARY; PRT; 1951 AA.
AC Q17042;
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE MYOSIN HEAVY CHAIN.
OS Aequipecten irradians (Bay scallop).
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Pectinoidea;
OC Pectinoidea; Pectinidae; Argopecten.
OX NCBI_TaxID=31199;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=MUSCLE, CATCH (SMOOTH) ADDUCTOR;
RX MEDLINE=95108023; Pubmed=7809102;
RA Nyitrai L., Jancso A., Ochialy V., Graf L., Szent-Gyorgyi A.G.;
RT "scallop striated and smooth muscle myosin heavy-chain isoforms are
RT produced by alternative RNA splicing from a single gene.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:12686-12690(1994).
DR EMBL: U09782; AAC64690.1; -.
DR HSSP: P24733; 1WDC.
DR InterPro: IPR000048; IQ.
DR InterPro: IPR001609; myosin_head.
DR InterPro: IPR004009; Myosin_N.
DR InterPro: IPR002928; Myosin_tail.
DR Pfam: PF00612; IQ; 2.
DR Pfam: PF00063; myosin_head; 1.

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DR Pfam: PF02736; Myosin_N; 1.
DR Pfam: PF01576; Myosin_tail; 1.
DR PRINTS: PR00193; MYOSINHEAVY.
DR ProDom: PD000355; myosin_head; 1.
DR SMART: SM00015; IQ; 1.
DR SMART: SM00242; MYSC; 1.
DR PROSITE: PS50096; IQ; 1.
SQ SEQUENCE 1951 AA; 224253 MW; 1FDC3D7D691C1410 CRC64;

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Query Match 15.1%; Score 162; DB 5; Length 1951;
Best Local Similarity 24.5%; Pred. No. 0.28; Mismatches 89; Indels 86; Gaps 12;
Matches 73; Conservative 50;

QY 1 KTIINKLFFD-----LAQEEENVLDAEFLKNEIDSVKAQL-----SOK 38
DB 907 KLIMQKADFESEQIKELERLDEDAADLEGIKKMEADANLKDIDGDLNTLOKAEQ 966
QY 39 DREKRSQAIIIDL-----RDTLEERN-ATVESLO-----NALNKA 74
DB 967 DKAKKDNO--ISTLQGISQODEHIGKLNKKEKALEANKKTSLSLAEDKCNHLNK-- 1022
QY 75 MLCSTLKKOMKFLERODETKQAREEAHRLCKMK-----TMEQIELLLQSORSEVEEMI 129
DB 1023 -LKAKLEQALDELNDNEREKKVGDEYKAKRKVEQDLKSTQENVEDLERVKR-ELLEENV 1080
QY 130 R-----DMVGQSAVEQLAVYCVSLKKEYENLKEARKATGELADRLKDLVSSR 178
DB 1081 RRKEAEISLNSKLEEDONLVSQLQRIKELQARIEELEELAEARNARAVEQKORAEIN 1140
QY 179 SKLTLNTELDQA-----KLELRSQOKDLSA-----DOETISLRKSSD 218
DB 1141 RELEELGERLDEAGATSAQIELNKKRPAELIKIRDLLEASLOHEAOISALRRKHOD 1198

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Search completed: September 4, 2002, 16:16:07  
 Job time: 1491 sec

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